

IN THE SPECIFICATION:

Please delete the Sequence Listing of record and insert the substitute Sequence Listing provided herewith in the above-identified application.

REMARKS

In response to the Office Communication dated September 26, 2001 and in accordance with the provisions in 37 C.F.R. §1.821-§1.825, Applicants submit herewith a substitute paper and an initial computer readable copy of the Sequence Listing, along with a Statement Under 37 C.F.R. §1.821(f), stating that these copies are identical. A copy of the Notice to Comply is also enclosed.

The substitute Sequence Listing is compiled using Patent In Version 2.1. Applicants have also corrected certain typographical errors in the original Sequence Listing. More specifically, Applicants have made corrections in the section of total length in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 6 and SEQ ID NO: 7 to reflect the correct length of these molecules. In addition, Applicants have corrected a typographical error in the sequence of SEQ ID NO: 7 at nucleotide number 505-507: the codon "TGA" has been replaced with "TCA". It is respectfully submitted that those skilled in the art would have readily recognized the stop codon "TGA" in the original Sequence Listing of SEQ ID NO: 7 to be an obvious typographical error. As described in the specification at page 8, lines 7-24, SEQ ID NO: 7 is a derivative of the murine *bcl-w* sequence as set forth in SEQ ID NO: 3. Thus, those skilled in the art would have looked to SEQ ID NO: 3 (murine *bcl-w*) and would have recognized that the codon TGA should

read "TCA" instead. Similarly, the symbol "*" (representing stop codon encoded by TGA) in SEQ ID NO: 8 should read "Ser" (encoded by the codon TCA).

It is respectfully submitted that the above amendment to the Sequence Listing does not introduce new matter. A marked-up version of the Sequence Listing is enclosed to show the changes made. Applicants have also amended the specification to insert the substitute Sequence Listing.

In view of the foregoing Amendment and the Remarks, it is believed that the subject case is in condition for an examination on the merits, which action is earnestly solicited.

Respectfully submitted,



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Enclosures:

- Marked-up version of the Sequence Listing;
- Statement Under 37 C.F.R. §1.821(f);
- Copy of the Notice to Comply.



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SEQUENCE LISTING

(I) GENERAL INFORMATION:

- (i) APPLICANT: (US ONLY): S. CORY, J.A. ADAMS, C. PRINT, L. GIBSON
(OTHER THAN US) THE WALTER AND ELIZA HALL INSTITUTE
OF MEDICAL RESEARCH
- (ii) TITLE OF INVENTION: A METHOD OF TREATMENT AND AN ANIMAL
MODEL USEFUL FOR SAME
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: DAVIES COLLISON CAVE
 - (B) STREET: 1 LITTLE COLLINS STREET
 - (C) CITY: MELBOURNE
 - (D) STATE: VICTORIA
 - (E) COUNTRY: AUSTRALIA
 - (F) ZIP: 3000
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT INTERNATIONAL
 - (B) FILING DATE: 16-SEP-1998
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PO9228
 - (B) FILING DATE: 16-SEP-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: HUGHES, DR E JOHN L
 - (C) REFERENCE/DOCKET NUMBER: EJH/EK
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: +61 3 9254 2777
 - (B) TELEFAX: +61 3 9254 2770
 - (C) TELEX: AA 31787

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: ~~688~~ base pairs 581
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..~~582~~ 579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GCG ACC CCA GCC TCG GCC CCA GAC ACA CGG GCT CTG GTG GCA GAC	48
Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp	
1 5 10 15	
TTT GTA GGT TAT AAG CTG AGG CAG AAG GGT TAT GTC TGT GGA GCT GGC	96
Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly	
20 25 30	
CCC GGG GAG GGC CCA GCA GCT GAC CCG CTG CAC CAA GCC ATG CGG GCA	144
Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala	
35 40 45	
GCT GGA GAT GAG TTC GAG ACC CGC TTC CGG CGC ACC TTC TCT GAT CTG	192
Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu	
50 55 60	
GCG GCT CAG CTG CAT GTG ACC CCA GGC TCA GCC CAA CAA CGC TTC ACC	240
Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr	
65 70 75 80	
CAG GTC TCC GAT GAA CTT TTT CAA GGG GGC CCC AAC TGG GGC CGC CTT	288
Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu	
85 90 95	
GTA GCC TTC TTT GTC TTT GGG GCT GCA CTG TGT GCT GAG AGT GTC AAC	336
Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn	
100 105 110	
AAG GAG ATG GAA CCA CTG GTG GGA CAA GTG CAG GAG TGG ATG GTG GCC	384
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala	
115 120 125	
TAC CTG GAG ACG CGG CTG GCT GAC TCG ATC CAC AGC AGT GGG GGC TGG	432
Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp	
130 135 140	
GCG GAG TTC ACA GCT CTA TAC GGG GAC GGG GCC CTG GAG GAG GCG CGG	480
Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg	
145 150 155 160	
CGT CTG CGG GAG GGG AAC TGG GCA TCA GTG AGG ACA GTG CTG ACG GGG	528
Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly	
165 170 175	
GCC GTG GCA CTG GGG GCC CTG GTA ACT GTA GGG GCC TTT TTT GCT AGC	576
Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser	
180 185 190	
AAG TG	
Lys	

[582]

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp
 1           5           10           15
Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
      20           25           30
Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
      35           40           45
Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
      50           55           60
Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
      65           70           75           80
Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
      85           90           95
Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
      100          105          110
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
      115          120          125
Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
      130          135          140
Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
      145          150          155          160
Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
      165          170          175
Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
      180          185          190

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Lys

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(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 582 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GCG ACC CCA GCC TCA ACC CCA GAC ACA CGG GCT CTA GTG GCT GAC	49
Met Ala Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp	
1 5 10 15	
TTT GTA GGC TAT AAG CTG AGG CAG AAG GGT TAT GTC TGT GGA GCT GGC	96
Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly	
20 25 30	
CCT GGG GAA GGC CCA GCC GCC GAC CCG CTG CAC CAA GCC ATG CGG GCT	144
Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala	
35 40 45	
GCT GGA GAC GAG TTT GAG ACC CGT TTC CGC CGC ACC TTC TCT GAC CTG	192
Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu	
50 55 60	
GCC GCT CAG CTA CAC GTG ACC CCA GGC TCA GCC CAG CAA CGC TTC ACC	240
Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr	
65 70 75 80	
CAG GTT TCC GAC GAA CTT TTC CAA GGG GGC CCT AAC TGG GGC CGT CTT	288
Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu	
85 90 95	
GTG GCA TTC TTT GTC TTT GGG GCT GCC CTG TGT GCT GAG AGT GTC AAC	336
Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn	
100 105 110	
AAA GAA ATG GAG CCT TTG GTG GGA CAA GTG CAG GAT TGG ATG GTG GCC	384
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Met Val Ala	
115 120 125	
TAC CTG GAG ACA CGT CTG GCT GAC TGG ATC CAC AGC AGT GGG GGC TGG	432
Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp	
130 135 140	
GCG GAG TTC ACA GCT CTA TAC GGG GAC GGG GCC CTG GAG GAG GCA CGG	480
Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg	
145 150 155 160	
CGT CTG CGG GAG GGG AAC TGG GCA TCA GTG AGG ACA GTG CTG ACG GGG	528
Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly	
165 170 175	
GCC GTG GCA CTG GGG GCC CTG GTA ACT GTA GGG GCC TTT TTT GCT AGC	576
Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser	
180 185 190	

AAG TG
 Lys

[582] 581

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Ala Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp
 1           5           10           15
Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
 20           25           30
Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
 35           40           45
Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
 50           55           60
Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
 65           70           75           80
Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
 85           90           95
Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
100          105          110
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Met Val Ala
115          120          125
Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
130          135          140
Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
145          150          155          160
Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
165          170          175
Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
180          185          190

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Lys

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..583

579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG GCG ACC CCA GCC TCG GCC CCA GAC ACA CGG GCT CTG GTG GCA GAC	48
Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp	
1 5 10 15	
TTT GTA GGT TAT AAG CTG AGG CAG AAG GGT TAT GTC TGT GGA GCT GGC	96
Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly	
20 25 30	
CCC GGG GAG GGC CCA GCA GCT GAC CCG CTG CAC CAA GCC ATG CGG GCA	144
Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala	
35 40 45	
GCT GGA GAT GAG TTC GAG ACC CGC TTC CGG CGC ACC TTC TCT GAT CTG	192
Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu	
50 55 60	
GCG GCT CAG CTG CAT GTG ACC CCA GGC TCA GCC CAG CAA CGC TTC ACC	240
Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr	
65 70 75 80	
CAG GTC TCC GAC GAA CTT TTT CAA GGG GGC CCC AAC TGG GGC CGC CTT	288
Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu	
85 90 95	
GTA GCC TTC TTT CTC TTT GGG GCT GCA CTG TGT GCT GAG AGT GTC AAC	336
Val Ala Phe Phe Leu Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn	
100 105 110	
AAG GAG ATG GAA CCA CTG GTG GGA CAA GTG CAG GAG TGG ATG GTG GCC	384
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala	
115 120 125	
TAC CTG GAG ACG CGG CTG GTC GAC TGG ATC CAC AGC AGT GGG GGC TGG	432
Tyr Leu Glu Thr Arg Leu Val Asp Trp Ile His Ser Ser Gly Gly Trp	
130 135 140	
GCG GAG TTC ACA GCT CTA TAC GGG GAC GGG GCC CTG GAG GAG GCG CGG	480
Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg	
145 150 155 160	
CGT CTG CGG GAG GGG AAC TGG GCA TCA GTG AGG ACA GTG CTG ACG GGG	528
Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly	
165 170 175	
GCC GTG GCA CTG GGG GCC CTG GTA ACT GTA GGG GCC TTT TTT GCT AGC	576
Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser	
180 185 190	
AAG TGA A	583
Lys	

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: ¹⁹³194 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp
 1           5           10           15
Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
      20           25           30
Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
      35           40           45
Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
      50           55           60
Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
      65           70           75           80
Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
      85           90           95
Val Ala Phe Phe Leu Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
      100          105          110
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
      115          120          125
Tyr Leu Glu Thr Arg Leu Val Asp Trp Ile His Ser Ser Gly Gly Trp
      130          135          140
Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
      145          150          155          160
Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
      165          170          175
Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
      180          185          190

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Lys

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(2) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATG CCG ACC CCA GCC TCA ACC CCA GAC ACA CGC GCT CTA GTG GCT GAC	48
Met Pro Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp	
1 5 10 15	
TTT GTA GGC TAT AGG CTG AGG CAG AAG GGT TAT GTC TGT GGA GCT GGG	96
Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly	
20 25 30	
CCT GGG GAA GGC CCA GCC GCC GAC CCG CTG CAC CAA GCC ATG CGG GCT	144
Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala	
35 40 45	
GCT GGA GAC GAG TTT GAG ACC CGT TTC CGC CGC ACC TTC TCT GAC CTG	192
Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu	
50 55 60	
GCC GCT CAG CTA CAC GTG ACC CCA GGC TCA GCC CAG CAA CGC TTC ACC	240
Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr	
65 70 75 80	
CAG GTT TCC GAC GAA CTT TTC CAA GGG GGC CCT AAC TGG GGC CGT CTT	288
Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu	
85 90 95	
GTG GCA TTC TTT GTC TTT GGG GCT GCC CTG TGT GCT GAG AGT GTC AAC	336
Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn	
100 105 110	
AAA GAA ATG GAG CCT TTG GTG GGA CAA GTC CAG GAT TGG ATC GTG GCC	384
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Ile Val Ala	
115 120 125	
TAC CTG GAG ACA CGT CTG GCT GAC TGG ATC CAC AGC AGT GGC GGC TGG	432
Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp	
130 135 140	
GCG GAC TTC ACA GCT CTA TAC GGG GAC GGG GCC CTG GAG GAC GCA CGG	480
Ala Asp Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Asp Ala Arg	
145 150 155 160	
CGT CTG CGG GAG GGC AAC TGG GCA TGA GTG AGC ACA GTG GTG ACG GGG	528
Arg Leu Arg Glu Gly Asn Trp Ala Val Ser Thr Val Val Thr Gly	
165 170 175	
GCC GTG GCA CTG GGG GCC CTG GTA ACT GTA GGG GCC TTT TTT GCT AGC	576
Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser	
180 185 190	
AAG TG	
Lys	

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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Pro Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp
 1 5 10 15
 Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
 20 25 30
 Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
 35 40 45
 Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
 50 55 60
 Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
 65 70 75 80
 Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
 85 90 95
 Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
 100 105 110
 Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Ile Val Ala
 115 120 125
 Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
 130 135 140
 Ala Asp Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Asp Ala Arg
 145 150 155 160
 Arg Leu Arg Glu Gly Asn Trp Ala Val Ser Thr Val Val Thr Gly
 165 170 175
 Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
 180 185 190

Lys